

C. L. autman

1646

#3

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/339,153A

DATE: 09/10/1999
TIME: 15:09:44

INPUT SET: S33278.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information

- (i) APPLICANT: Lok, Si
Adams, Robyn L.
Jelmsberg, Anna C.
Whitmore, Theodore E.
Farrah, Theresa M.
- (ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR11
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Zymogenetics
 - (B) STREET: 1201 Eastlake Ave East
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98102
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lunn, Paul G
 - (B) REGISTRATION NUMBER: 32,743
 - (C) REFERENCE/DOCKET NUMBER: 97-52
- (ix) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: 206-442-6627
48 (B) TELEFAX: 206-442-6678
49 (C) TELEX:

50
51
52 (2) INFORMATION FOR SEQ ID NO:1:
53

54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 2831 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear

59
60 (ii) MOLECULE TYPE: cDNA
61 (ix) FEATURE:

62
63 (A) NAME/KEY: Coding Sequence
64 (B) LOCATION: 34...1755
65 (D) OTHER INFORMATION:
66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68

69	TAGAGGCCAA GGGAGGGCTC TGTGCCAGCC CCG ATG AGG ACG CTG CTG ACC ATC	54
70	Met Arg Thr Leu Leu Thr Ile	
71	1 5	
72		
73	TTG ACT GTG GGA TCC CTG GCT GCT CAC GCC CCT GAG GAC CCC TCG GAT	102
74	Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp	
75	10 15 20	
76		
77	CTG CTC CAG CAC GTG AAA TTC CAG TCC AGC AAC TTT GAA AAC ATC CTG	150
78	Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu	
79	25 30 35	
80		
81	ACG TGG GAC AGC GGG CCA GAG GGC ACC CCA GAC ACG GTC TAC AGC ATC	198
82	Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile	
83	40 45 50 55	
84		
85	GAG TAT AAG ACG TAC GGA GAG AGG GAC TGG GTG GCA AAG AAG GGC TGT	246
86	Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys	
87	60 65 70	
88		
89	CAG CGG ATC ACC CGG AAG TCC TGC AAC CTG ACG GTG GAG ACG GGC AAC	294
90	Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn	
91	75 80 85	
92		
93	CTC ACG GAG CTC TAC TAT GCC AGG GTC ACC GCT GTC AGT GCG GGA GGC	342
94	Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly	
95	90 95 100	
96		
97	CGG TCA GCC ACC AAG ATG ACT GAC AGG TTC AGC TCT CTG CAG CAC ACT	390
98	Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr	
99	105 110 115	

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100																		
101	ACC	CTC	AAG	CCA	CCT	GAT	GTG	ACC	TGT	ATC	TCC	AAA	GTG	AGA	TCG	ATT		438
102	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile		
103	120					125					130					135		
104																		
105	CAG	ATG	ATT	GTT	CAT	CCT	ACC	CCC	ACG	CCA	ATC	CGT	GCA	GGC	GAT	GGC		486
106	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly		
107					140					145					150			
108																		
109	CAC	CGG	CTA	ACC	CTG	GAA	GAC	ATC	TTC	CAT	GAC	CTG	TTC	TAC	CAC	TTA		534
110	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu		
111				155					160					165				
112																		
113	GAG	CTC	CAG	GTC	AAC	CGC	ACC	TAC	CAA	ATG	CAC	CTT	GGA	GGG	AAG	CAG		582
114	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln		
115			170					175					180					
116																		
117	AGA	GAA	TAT	GAG	TTC	TTC	GGC	CTG	ACC	CCT	GAC	ACA	GAG	TTC	CTT	GGC		630
118	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly		
119		185					190				195							
120																		
121	ACC	ATC	ATG	ATT	TGC	GTT	CCC	ACC	TGG	GCC	AAG	GAG	AGT	GCC	CCC	TAC		678
122	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr		
123	200					205				210						215		
124																		
125	ATG	TGC	CGA	GTG	AAG	ACA	CTG	CCA	GAC	CGG	ACA	TGG	ACC	TAC	TCC	TTC		726
126	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe		
127					220				225						230			
128																		
129	TCC	GGA	GCC	TTC	CTG	TTC	TCC	ATG	GGC	TTC	CTC	GTC	GCA	GTA	CTC	TGC		774
130	Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys		
131				235					240					245				
132																		
133																		
134	TAC	CTG	AGC	TAC	AGA	TAT	GTC	ACC	AAG	CCG	CCT	GCA	CCT	CCC	AAC	TCC		822
135	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser		
136			250					255					260					
137																		
138	CTG	AAC	GTC	CAG	CGA	GTC	CTG	ACT	TTC	CAG	CCG	CTG	CGC	TTC	ATC	CAG		870
139	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln		
140		265					270					275						
141																		
142	GAG	CAC	GTC	CTG	ATC	CCT	GTC	TTT	GAC	CTC	AGC	GGC	CCC	AGC	AGT	CTG		918
143	Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu		
144	280					285					290					295		
145																		
146	GCC	CAG	CCT	GTC	CAG	TAC	TCC	CAG	ATC	AGG	GTG	TCT	GGA	CCC	AGG	GAG		966
147	Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu		
148					300					305					310			
149																		
150	CCC	GCA	GGA	GCT	CCA	CAG	CGG	CAT	AGC	CTG	TCC	GAG	ATC	ACC	TAC	TTA		1014
151	Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu		
152				315					320					325				

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/339,153ADATE: 09/10/1999
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206
207 CTT GTG TGT CCC AAG GAT GAA GCC AAG AGC CCA GCC CCT GAG ACC TCA 1686
208 Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
209          540          545          550
210
211 GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC 1734
212 Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
213          555          560          565
214
215 CTG ACT GTG CAG TGG GAG TCC TGAGGGGAAT GGGAAAGGCT TGGTGCTTCC TCCC 1789
216 Leu Thr Val Gln Trp Glu Ser
217          570
218
219 TGTCCCTACC CAGTGTACACA TCCTTGGCTG TCAATCCCAT GCCTGCCCCAT GCCACACACT 1849
220 CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAAGCAG AGGGAGTGGC ATGCAGGGCC 1909
221 CCTGCCATGG GTGCGCTCCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCGGGGGA 1969
222 GCTCTGGGGA GCAGCTTGTG TAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT 2029
223 GACAGTGCAA GGAGGAAATG CAGGGAAACT CCCGAGGTCC AGAGCCCCAC CTCCTAACAC 2089
224 CATGGATTCA AAGTGCTCAG GGAATTTGCC TCTCCTTGCC CCATTCTTGG CCAGTTTCAC 2149
225 AATCTAGCTC GACAGAGCAT GAGGCCCTG CCTCTTCTGT CATTGTTCAA AGGTGGGAAG 2209
226 AGAGCCTGGA AAAGAACCAG GCCTGGAAAA GAACCAGAAG GAGGCTGGGC AGAACCAGAA 2269
227 CAACCTGCAC TTCTGCCAAG GCCAGGGCCA GCAGGACGGC AGGACTCTAG GGAGGGGTGT 2329
228 GGCCTGCAGC TCATTCCCAG CCAGGGCAAC TGCCTGACGT TGCACGATTT CAGCTTCATT 2389
229 CCTCTGATAG AACAAAGCGA AATGCAGGTC CACCAGGGAG GGAGACACAC AAGCCTTTTC 2449
230 TGCAGGCAGG AGTTTCAGAC CCTATCCTGA GAATGGGGTT TGAAAGGAAG GTGAGGGCTG 2509
231 TGGCCCCTGG ACGGGTACAA TAACACACTG TACTGATGTC ACAACTTTGC AAGCTCTGCC 2569
232 TTGGGTTTCTG CCCATCTGGG CTCAAATTCC AGCCTCACCA CTCACAAGCT GTGTGACTTC 2629
233 AAACAAATGA AATCAGTGCC CAGAACCTCG GTTTCCTCAT CTGTAATGTG GGGATCATAA 2689
234 CACCTACCTC ATGGAGTTGT GGTGAAGATG AAATGAAGTC ATGTCTTTAA AGTGCTTAAT 2749
235 AGTGCCTGGT ACATGGGCAG TGCCCAATAA ACGGTAGCTA TTTAAAAAAA AAAAAAAAAA 2809
236 AAAAAAATAG CGGCCGCCTC GA 2831
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
250
251 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
252   1           5           10           15
253 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
254          20          25          30
255 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
256          35          40          45
257 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
258          50          55          60
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SEQUENCE VERIFICATION REPORT
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